RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/552,515 _____

Source: _____ PCT _____

Date Processed by STIC: _____ 10/20/2005 _____

ENTERED

RAW SEQUENCE LISTING   DATE: 10/20/2005
PATENT APPLICATION: US/10/552,515   TIME: 09:40:29

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\10202005\J552515.raw

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 3 <110> APPLICANT: The Government of the United States of America as
 4       represented by the Secretary of the Department of Health and
 5       Human Services
 6       Bera, Tapan K.
 7       Pastan, Ira H.
 8       Lee, Byungkook
10 <120> TITLE OF INVENTION: GENE EXPRESSED IN PROSTATE CANCER AND METHODS OF USE
12 <130> FILE REFERENCE: 4239-68223-02
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/552,515
C--> 14 <141> CURRENT FILING DATE: 2005-10-06
14 <150> PRIOR APPLICATION NUMBER: PCT/US2004/10588
15 <151> PRIOR FILING DATE: 2004-04-05
17 <150> PRIOR APPLICATION NUMBER: 60/461,399
18 <151> PRIOR FILING DATE: 2003-04-08
20 <160> NUMBER OF SEQ ID NOS: 12
22 <170> SOFTWARE: PatentIn version 3.2
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 933
26 <212> TYPE: PRT
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
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42 Ala His Ala Glu Arg Trp Ala Met Thr Ser Glu Thr Ser Ser Gly Ser
43         35                  40                  45
46 His Cys Ala Arg Ser Arg Met Leu Arg Arg Arg Ala Gln Glu Glu Asp
47     50                  55                  60
50 Ser Thr Val Leu Ile Asp Val Ser Pro Pro Glu Ala Glu Lys Arg Gly
51 65                  70                  75                  80
54 Ser Tyr Gly Ser Thr Ala His Ala Ser Glu Pro Gly Gly Gln Gln Ala
55              85                  90                  95
58 Ala Ala Cys Arg Ala Gly Ser Pro Ala Lys Pro Arg Ile Ala Asp Phe
59             100                 105                 110
62 Val Leu Val Trp Glu Glu Asp Leu Lys Leu Asp Arg Gln Gln Asp Ser
63             115                 120                 125
66 Ala Ala Arg Asp Arg Thr Asp Met His Arg Thr Trp Arg Glu Thr Phe
67         130                 135                 140
70 Leu Asp Asn Leu Arg Ala Ala Gly Leu Cys Val Asp Gln Gln Asp Val
71 145                 150                 155                 160
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74  Gln Asp Gly Asn Thr Thr Val His Tyr Ala Leu Leu Ser Ala Ser Trp
75              165                 170                 175
78  Ala Val Leu Cys Tyr Tyr Ala Glu Asp Leu Arg Leu Lys Leu Pro Leu
79              180                 185                 190
82  Gln Glu Leu Pro Asn Gln Ala Ser Asn Trp Ser Ala Gly Leu Leu Ala
83              195                 200                 205
86  Trp Leu Gly Ile Pro Asn Val Leu Leu Glu Val Val Pro Asp Val Pro
87          210                 215                 220
90  Pro Glu Tyr Tyr Ser Cys Arg Phe Arg Val Asn Lys Leu Pro Arg Phe
91  225                 230                 235                 240
94  Leu Gly Ser Asp Asn Gln Asp Thr Phe Phe Thr Ser Thr Lys Arg His
95              245                 250                 255
98  Gln Ile Leu Phe Glu Ile Leu Ala Lys Thr Pro Tyr Gly His Glu Lys
99              260                 265                 270
102 Lys Asn Leu Leu Gly Ile His Gln Leu Leu Ala Glu Gly Val Leu Ser
103             275                 280                 285
106 Ala Ala Phe Pro Leu His Asp Gly Pro Phe Lys Thr Pro Pro Glu Gly
107         290                 295                 300
110 Pro Gln Ala Pro Arg Leu Asn Gln Arg Gln Val Leu Phe Gln His Trp
111 305                 310                 315                 320
114 Ala Arg Trp Gly Lys Trp Asn Lys Tyr Gln Pro Leu Asp His Val Arg
115             325                 330                 335
118 Arg Tyr Phe Gly Glu Lys Val Ala Leu Tyr Phe Ala Trp Leu Gly Phe
119             340                 345                 350
122 Tyr Thr Gly Trp Leu Leu Pro Ala Ala Val Val Gly Thr Leu Val Phe
123         355                 360                 365
126 Leu Val Gly Cys Phe Leu Val Phe Ser Asp Ile Pro Thr Gln Glu Leu
127         370                 375                 380
130 Cys Gly Ser Lys Asp Ser Phe Glu Met Cys Pro Leu Cys Leu Asp Cys
131 385                 390                 395                 400
134 Pro Phe Trp Leu Leu Ser Ser Ala Cys Ala Leu Ala Gln Ala Gly Arg
135             405                 410                 415
138 Leu Phe Asp His Gly Gly Thr Val Phe Phe Ser Leu Phe Met Ala Leu
139             420                 425                 430
142 Trp Ala Val Leu Leu Leu Glu Tyr Trp Lys Arg Lys Ser Ala Thr Leu
143         435                 440                 445
146 Ala Tyr Arg Trp Asp Cys Ser Asp Tyr Glu Asp Thr Glu Glu Arg Pro
147         450                 455                 460
150 Arg Pro Gln Phe Ala Ala Ser Ala Pro Met Thr Ala Pro Asn Pro Ile
151 465                 470                 475                 480
154 Thr Gly Glu Asp Glu Pro Tyr Phe Pro Glu Arg Ser Arg Ala Arg Arg
155             485                 490                 495
158 Met Leu Ala Gly Ser Val Val Ile Val Val Met Val Ala Val Val Val
159             500                 505                 510
162 Met Cys Leu Val Ser Ile Ile Leu Tyr Arg Ala Ile Met Ala Ile Val
163         515                 520                 525
166 Val Ser Arg Ser Gly Asn Thr Leu Leu Ala Ala Trp Ala Ser Arg Ile
167         530                 535                 540
170 Ala Ser Leu Thr Gly Ser Val Val Asn Leu Val Phe Ile Leu Ile Leu
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171 545                  550                  555                  560
174 Ser Lys Ile Tyr Val Ser Leu Ala His Val Leu Thr Arg Trp Glu Met
175                  565                  570                  575
178 His Arg Thr Gln Thr Lys Phe Glu Asp Ala Phe Thr Leu Lys Val Phe
179                  580                  585                  590
182 Ile Phe Gln Phe Val Asn Phe Tyr Ser Ser Pro Val Tyr Ile Ala Phe
183                  595                  600                  605
186 Phe Lys Gly Arg Phe Val Gly Tyr Pro Gly Asn Tyr His Thr Leu Phe
187          610                  615                  620
190 Gly Val Arg Asn Glu Glu Cys Ala Ala Gly Gly Cys Leu Ile Glu Leu
191 625                  630                  635                  640
194 Ala Gln Glu Leu Leu Val Ile Met Val Gly Lys Gln Val Ile Asn Asn
195                  645                  650                  655
198 Met Gln Glu Val Leu Ile Pro Lys Leu Lys Gly Trp Trp Gln Lys Phe
199                  660                  665                  670
202 Arg Leu Arg Ser Lys Lys Arg Lys Ala Gly Ala Ser Ala Gly Ala Ser
203          675                  680                  685
206 Gln Gly Pro Trp Glu Asp Asp Tyr Glu Leu Val Pro Cys Glu Gly Leu
207          690                  695                  700
210 Phe Asp Glu Tyr Leu Glu Met Val Leu Gln Phe Gly Phe Val Thr Ile
211 705                  710                  715                  720
214 Phe Val Ala Ala Cys Pro Leu Ala Pro Leu Phe Ala Leu Leu Asn Asn
215                  725                  730                  735
218 Trp Val Glu Ile Arg Leu Asp Ala Arg Lys Phe Val Cys Glu Tyr Arg
219                  740                  745                  750
222 Arg Pro Val Ala Glu Arg Ala Gln Asp Ile Gly Ile Trp Phe His Ile
223          755                  760                  765
226 Leu Ala Gly Leu Thr His Leu Ala Val Ile Ser Asn Ala Phe Leu Leu
227          770                  775                  780
230 Ala Phe Ser Ser Asp Phe Leu Pro Arg Ala Tyr Tyr Arg Trp Thr Arg
231 785                  790                  795                  800
234 Ala His Asp Leu Arg Gly Phe Leu Asn Phe Thr Leu Ala Arg Ala Pro
235                  805                  810                  815
238 Ser Ser Phe Ala Ala Ala His Asn Arg Thr Cys Arg Tyr Arg Ala Phe
239                  820                  825                  830
242 Arg Asp Asp Asp Gly His Tyr Ser Gln Thr Tyr Trp Asn Leu Leu Ala
243          835                  840                  845
246 Ile Arg Leu Ala Phe Val Ile Val Phe Glu His Val Val Phe Ser Val
247          850                  855                  860
250 Gly Arg Leu Leu Asp Leu Leu Val Pro Asp Ile Pro Glu Ser Val Glu
251 865                  870                  875                  880
254 Ile Lys Val Lys Arg Glu Tyr Tyr Leu Ala Lys Gln Ala Leu Ala Glu
255                  885                  890                  895
258 Asn Glu Val Leu Phe Gly Thr Asn Gly Thr Lys Asp Glu Gln Pro Lys
259                  900                  905                  910
262 Gly Ser Glu Leu Ser Ser His Trp Thr Pro Phe Thr Val Pro Lys Ala
263          915                  920                  925
266 Ser Gln Leu Gln Gln
267          930
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PATENT APPLICATION: US/10/552,515   TIME: 09:40:29

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271 <211> LENGTH: 3308
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
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283 ctgcctgggc ggggctccaa gggccacccc tccccaccct ctgtcccgca gtgaggacgg    180
285 gactctactg ccgagaccag gctcacgctg agaggtgggc catgacctcc gagacctctt    240
287 ccggaagcca ctgtgccagg agcaggatgc tgcggcgacg ggcccaggaa gaggacagca    300
289 ccgtcctgat cgatgtgagc cccctgagg cagagaagag gggctcttac gggagcacag    360
291 cccacgcctc ggagccaggt ggacagcaag cggccgcctg cagagctggg agtcctgcca    420
293 agccccggat cgcagacttc gtcctcgttt gggaggagga cctgaagcta gacaggcagc    480
295 aggacagtgc cgcccgggac agaacagaca tgcacaggac ctggcgggag acttttctgg    540
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299 cagtgcacta cgccctcctc agcgcctcct gggctgtgct ctgctactac gccgaagacc    660
301 tgcgcctgaa gctgcccttg caggagttac ccaaccaggc ctccaactgg tcggccggcc    720
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307 aggacacctt cttcacaagc accaagaggc accaaattct gtttgagatc ctggccaaga    900
309 ccccgtatgg ccacgagaag aaaaacctgc ttgggatcca ccagctgctg gcagagggtg    960
311 tcctcagtgc cgccttcccc ctgcatgacg gccccttcaa gacgccccca gagggcccgc   1020
313 aggctccacg cctcaaccag cgccaagtcc ttttccagca ctgggcgcgc tggggcaagt   1080
315 ggaacaagta ccagcccctg gaccacgtgc gcaggtactt cggggagaag gtggccctct   1140
317 acttcgcctg gctcgggttt tacacaggct ggctcctgcc agcggcagtg gtgggcacac   1200
319 tggtgttcct ggtgggctgc ttcctggtgt tctcagacat acccacgcag gaactgtgtg   1260
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337 gcctcacggg gtctgtagtg aacctcgtct tcatcctcat cctctccaag atctatgtat   1800
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341 ccttcaccct caaggtgttc atcttccagt tcgtcaactt ctactcctca cccgtctaca   1920
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347 tcatcatggt gggcaagcag gtcatcaaca acatgcagga ggtcctcatc ccgaagctaa   2100
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351 gggctagcca ggggccctgg gaggacgact atgagcttgt ccctgtgag ggtctgtttg   2220
353 acgagtacct ggaaatggtg ctgcagttcg gcttcgtcac catcttcgtg gccgcctgtc   2280
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363 gcttcctcaa cttcacgctg gcgcgagccc cgtcctcctt cgccgccgcg cacaaccgca   2580
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367 ttcttgccat ccgcctggcc ttcgtcattg tgtttgagca tgtggttttc tccgttggcc   2700
369 gcctcctgga cctcctggtg cctgacatcc cagagtctgt ggagatcaaa gtgaagcggg   2760
371 agtactacct ggctaagcag gcactggctg agaatgaggt tcttttggga acgaacggaa   2820
373 caaaggatga gcagcccaag ggctcagagc tcagctccca ctggacaccc ttcacggttc   2880
375 ccaaggccag ccagctgcag cagtgacgcc tggaaggaca tctggtggtc cttaggggag   2940
377 tggcccctcc tgagccctgc gagcagcgtc cttttcctct tccctcaggc agcggctgtg   3000
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381 cggcttctct cctcagagcg cctgtcactc catccccggc agggagggac cgtcagctca   3120
383 caaggccctc tttgtttcct gctcccagac ataagcccaa ggggcccctg cacccaaggg   3180
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393 <211> LENGTH: 9
394 <212> TYPE: PRT
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397 <220> FEATURE:
398 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
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409 <213> ORGANISM: Artificial Sequence
411 <220> FEATURE:
412 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
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417 1               5
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421 <211> LENGTH: 9
422 <212> TYPE: PRT
423 <213> ORGANISM: Artificial Sequence
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426 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
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435 <211> LENGTH: 9
436 <212> TYPE: PRT
437 <213> ORGANISM: Artificial Sequence
439 <220> FEATURE:
440 <223> OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate
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VERIFICATION SUMMARY   DATE: 10/20/2005
PATENT APPLICATION: **US/10/552,515**   TIME: 09:40:30

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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